# STIC Biotechnology Systems Branch

# RAW SEQUENCE LISTING
## ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/567,808_

Source: _LFWO_

Date Processed by STIC: _02/16/2006_

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**
**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY** or,
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
### http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

# Raw Sequence Listing Error Summary

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1____Wrapped Nucleics     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
     Wrapped Aminos     was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
        ·     prevent "wrapping."

2____Invalid Line Length     The rules require that a line **not exceed 72 characters** in length. This includes white spaces.

3____Misaligned Amino     The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
     Numbering     use **space characters**, instead.

4____Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
     ensure your subsequent submission is saved in ASCII text.**

5____Variable Length     Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
     each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
     residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
     "bug"     sequences(s) _____. Normally, PatentIn would automatically generate this section from the
     previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
     the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
     Artificial or Unknown sequences.**

7____Skipped Sequences     Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
     (OLD RULES)     (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
     (i)       SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
     This sequence is intentionally skipped

     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences     Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
     (NEW RULES)     <210> sequence id number
     <400> sequence id number
     000

9____Use of n's or Xaa's     Use of n's and/or Xaa's have been detected in the Sequence Listing.
     (NEW RULES)     Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
     In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10____Invalid <213>     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
     Response     scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
     is Artificial Sequence

11____Use of <220>     ~~Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.~~
     Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
     "Unknown." Please explain source of genetic material in <220> to <223> section.
     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
     "bug"     resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
     listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa     "n" can **only** represent a single underlined nucleotide; "Xaa" can **only** represent a single amino acid

RAW SEQUENCE LISTING                DATE: 02/16/2006
PATENT APPLICATION:  US/10/567,808      TIME: 12:55:34

Input Set : **A:\08321-0136PC.TXT**
Output Set: **N:\CRF4\02162006\J567808.raw**

```
 4 <110> APPLICANT: Thomas Jefferson University
 5       Albert J. Wong
 7 <120> TITLE OF INVENTION: METHOD FOR RAPID IDENTIFICATION OF
 8       ALTERNATIVE SPLICING
10 <130> FILE REFERENCE: 08321-0136PC
12 <140> CURRENT APPLICATION NUMBER: US/10/567,808
12 <141> CURRENT FILING DATE: 2006-02-08
12 <150> PRIOR APPLICATION NUMBER: 60/493,759
13 <151> PRIOR FILING DATE: 2003-08-08
15 <160> NUMBER OF SEQ ID NOS: 6
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 22
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <223> OTHER INFORMATION: selectable tag
27 <400> SEQUENCE: 1
28 gtcatgcata gcaattgtcg ac
30 <210> SEQ ID NO: 2
31 <211> LENGTH: 17
32 <212> TYPE: DNA
33 <213> ORGANISM: Artificial Sequence
35 <220> FEATURE:
36 <223> OTHER INFORMATION: selectable tag
38 <400> SEQUENCE: 2
39 tcccccgggg ggaatcg                                        17
41 <210> SEQ ID NO: 3
42 <211> LENGTH: 27
43 <212> TYPE: DNA
44 <213> ORGANISM: Artificial Sequence
46 <220> FEATURE:
47 <223> OTHER INFORMATION: selectable tag
49 <400> SEQUENCE: 3
50 atgcatagca acctcacgtg tgaatcg                             27
52 <210> SEQ ID NO: 4
53 <211> LENGTH: 21
54 <212> TYPE: DNA
55 <213> ORGANISM: Artificial Sequence
57 <220> FEATURE:
58 <223> OTHER INFORMATION: affinity medium
60 <400> SEQUENCE: 4
61 acacgtgagg ttgctatgca t                                  21
```

C--> 12 (lines 12 and 12 marked with "C-->" in left margin)

*Handwritten annotations:* Does Not Comply Corrected Diskette Needed CPR-1,2)

*Handwritten:* Invalid Response. What is the Source of genetic Material? P/s see Item #11 on error summary sheet

RAW SEQUENCE LISTING                    DATE: 02/16/2006
PATENT APPLICATION:  US/10/567,808      TIME: 12:55:34

Input Set : A:\08321-0136PC.TXT
Output Set: N:\CRF4\02162006\J567808.raw

63 <210> SEQ ID NO: 5
64 <211> LENGTH: 58
65 <212> TYPE: DNA
66 <213> ORGANISM: Artificial Sequence
68 <220> FEATURE:
69 <223> OTHER INFORMATION: polynucleotide linking moiety
71 <400> SEQUENCE: 5
72 acacgatccg cagatgtccg cagttattcc tttttggaa taactgcgga catctgcg      58
74 <210> SEQ ID NO: 6
75 <211> LENGTH: 30
76 <212> TYPE: DNA
77 <213> ORGANISM: Artificial Sequence
79 <220> FEATURE:
80 <223> OTHER INFORMATION: arbitrary sequence
82 <400> SEQUENCE: 6
83 aaattcctat gcatgctcaa tggactgtgt                                     30

*[handwritten: Same error]*

*[handwritten: Same error]*

**VERIFICATION SUMMARY**                     DATE: 02/16/2006
PATENT APPLICATION:  **US/10/567,808**        TIME: 12:55:35

Input Set : **A:\08321-0136PC.TXT**
Output Set: **N:\CRF4\02162006\J567808.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date